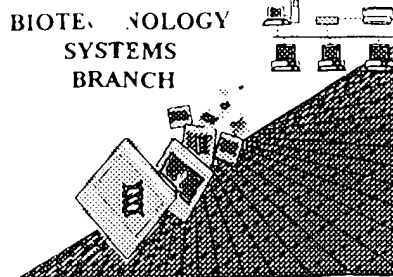


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/737,190
Source: OPE
Date Processed by STIC: 7/25/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST 25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/737,190

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
- 4 Non-ASCII
The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single **nucleotide** in a nucleic acid sequence. **N** is **not** used to represent any value not specifically a nucleotide.

OIKE

RAW SEQUENCE LISTING

DATE: 07/25/2001

PATENT APPLICATION: US/09/737,190

TIME: 13:05:30

Input Set : A:\14043.asc

Output Set: N:\CRF3\07252001\I737190.raw

Does Not Comply

Corrected Diskette Needed

4 <110> APPLICANT: Shibuya, Tetsuo
 6 <120> TITLE OF INVENTION: A Method for Changing a Target Array, a Method for Analyzing
 7 a Structure, and an Apparatus, a Storage Medium and a
 8 Transmission Medium Therefor
 10 <130> FILE REFERENCE: JP919990270US1 (14043)
 12 <140> CURRENT APPLICATION NUMBER: 09/737,190
 13 <141> CURRENT FILING DATE: 2000-12-14
 15 <160> NUMBER OF SEQ ID NOS: 2
 17 <170> SOFTWARE: PatentIn Ver. 2.1

ERRORED SEQUENCES

351 <210> SEQ ID NO: 2
 352 <211> LENGTH: 1334
 353 <212> TYPE: DNA
 354 <213> ORGANISM: Streptococcus anginosus
 356 <400> SEQUENCE: 2
 357 gaacgggtga gtaacgcgta ggtaacctgc ctattagagg gggataacta ttggaaacga 60
 359 tagctaatac cgcataacag tatgtaacac atgttagatg cttgaaagat gcaattgcat 120
 361 cgctagtaga tggacctgcg ttgtattagc tagtaggtag ggtaaaggcc tacctaggca 180
 363 acgatacata gccgacctga gaggggtgatc ggccacactg ggactgagac acggcccaga 240
 365 ctccacggg aggcagcagt agggaatctt cggcaatggg gggaaacctg accgagcaac 300
 367 gccgcgtgag tgaagaaggt ttccggatcg taaagctctg ttgttaagga agaacgagtg 360
 E--> 369 tgagaatgga aagttcatac tgtgacggta cttaaccaga aaggacggc tttactacgtg 420
 E--> 371 ccagcagccg cggtaatacg taggtccca gcgttgctcg gatttattgg gcgtaaagcg 480
 373 agcgcagggc gttagaaaag tctgaagtga aaggcagtg ctcaaccatt gtaggctttg 540
 375 gaaactgttt aacttgagtg cagaagggga gagtggaatt ccattgtgtg cgtgaaaatg 600
 377 cgtagatata tggaggaaca ccggtggcga aagcggctct ctggtctgta actgacgctg 660
 E--> 379 aggcctgaaa gcgtggggag cgaacaggat tagataccct ttttagtccac gccgtaaagc 720
 381 atgagtgtta ggtgttgggt cctttccggg actcagtgc gcagctaacg cattaagcac 780
 383 tccgcctggg gagtacgacc gcaaggttga aactcaaagg aattgacggg ggccgcacaa 840
 E--> 385 gcggtggagc atgttttta attcgaagga acgcgaagaa ccttaccagg tcttgacatc 900
 E--> 387 ccgatgcttt ttctagagat aggaagtctt ttcggaacat cggtgacagg tgggtgcatg 960
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 E--> 391 tgttagttgc catcattaag ttgggcactc tagcgagact gccggtaat aaccggagga 1080
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 395 tggtctgtac aacgagtcgc aagccggtga cggcaagcta atctctgaaa gccagtctca 1200
 E--> 397 gtccggtatt taggctgcaa ctgccttca tgaagtcgga atcgctagta atcgcgatc 1260
 E--> 399 agcacgccgc ggtgaatacg ttcccgggcc ttgtacacac cgcgcgtcac accacgagag 1320
 401 tttgtaacac ccga 1334

→ see item 9
 on Error
 Summary
 Sheet
 (error
 throughout
 seq. 2)

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/737,190

DATE: 07/25/2001

TIME: 13:05:31

Input Set : A:\14043.asc

Output Set: N:\CRF3\07252001\I737190.raw

L:369 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
M:340 Repeated in SeqNo=2